

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KLEIN, Michel H  
DU, Run-Pan  
EWASYSHYN, Mary E

(ii) TITLE OF INVENTION: INFECTION DETECTION METHOD USING  
CHIMERIC PROTEIN

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sim & McBurney  
(B) STREET: 6th Floor, 330 University Avenue  
(C) CITY: Toronto  
(D) STATE: Ontario  
(E) COUNTRY: Canada  
(F) ZIP: M5G 1R7

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/467,961  
(B) FILING DATE: 06-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/001,554  
(B) FILING DATE: 06-JAN-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9200117.1  
(B) FILING DATE: 06-JAN-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: STEWART, Michael I  
(B) REGISTRATION NUMBER: 24,973  
(C) REFERENCE/DOCKET NUMBER: 1038-1000 MIS:jb

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (416) 595-1155  
(B) TELEFAX: (416) 595-1163

(2) INFORMATION FOR SEQ ID NO:1:





145				150					155					160			
Val	Gln	Ser	Ser	Ile	Gly	Asn	Leu	Ile	Val	Ala	Ile	Lys	Ser	Val	Gln		
				165						170						175	
Asp	Tyr	Val	Asn	Asn	Glu	Ile	Val	Pro	Ser	Ile	Ala	Arg	Leu	Gly	Cys		
				180						185						190	
Glu	Ala	Ala	Gly	Leu	Gln	Leu	Gly	Ile	Ala	Leu	Thr	Gln	His	Tyr	Ser		
				195						200						205	
Glu	Leu	Thr	Asn	Ile	Phe	Gly	Asp	Asn	Ile	Gly	Ser	Leu	Gln	Glu	Lys		
				210						215						220	
Gly	Ile	Lys	Leu	Gln	Gly	Ile	Ala	Ser	Leu	Tyr	Arg	Thr	Asn	Ile	Thr		
				225						230						235	240
Glu	Ile	Phe	Thr	Thr	Ser	Thr	Val	Asp	Lys	Tyr	Asp	Ile	Tyr	Asp	Leu		
				245						250						255	
Leu	Phe	Thr	Glu	Ser	Ile	Lys	Val	Arg	Val	Ile	Asp	Val	Asp	Leu	Asn		
				260						265						270	
Asp	Tyr	Ser	Ile	Thr	Leu	Gln	Val	Arg	Leu	Pro	Leu	Leu	Thr	Arg	Leu		
				275						280						285	
Leu	Asn	Thr	Gln	Ile	Tyr	Lys	Val	Asp	Ser	Ile	Ser	Tyr	Asn	Ile	Gln		
				290						295						300	
Asn	Arg	Glu	Trp	Tyr	Ile	Pro	Leu	Pro	Ser	His	Ile	Met	Thr	Lys	Gly		
				305						310						315	320
Ala	Phe	Leu	Gly	Gly	Ala	Asp	Val	Lys	Glu	Cys	Ile	Glu	Ala	Phe	Ser		
				325						330						335	
Ser	Tyr	Ile	Cys	Pro	Ser	Asp	Pro	Gly	Phe	Val	Leu	Asn	His	Glu	Met		
				340						345						350	
Glu	Ser	Cys	Leu	Ser	Gly	Asn	Ile	Ser	Gln	Cys	Pro	Arg	Thr	Thr	Val		
				355						360						365	
Thr	Ser	Asp	Ile	Val	Pro	Arg	Tyr	Ala	Phe	Val	Asn	Gly	Gly	Val	Val		
				370						375						380	
Ala	Asn	Cys	Ile	Thr	Thr	Thr	Cys	Thr	Cys	Asn	Gly	Ile	Asp	Asn	Arg		
				385						390						395	400
Ile	Asn	Gln	Pro	Pro	Asp	Gln	Gly	Val	Lys	Ile	Ile	Thr	His	Lys	Glu		
				405						410						415	
Cys	Asn	Thr	Ile	Gly	Ile	Asn	Gly	Met	Leu	Phe	Asn	Thr	Asn	Lys	Glu		
				420						425						430	
Gly	Thr	Leu	Ala	Phe	Tyr	Thr	Pro	Asn	Asp	Ile	Thr	Leu	Asn	Asn	Ser		
				435						440						445	
Val	Ala	Leu	Asp	Pro	Ile	Asp	Ile	Ser	Ile	Glu	Leu	Asn	Lys	Ala	Lys		

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Ile	Ile	Val	Leu	Ile	Asn	Ser	Ile	Lys	Ser	Glu	Lys	Ala	His	Glu	Ser
50						55					60				
Leu	Leu	Gln	Asp	Ile	Asn	Asn	Glu	Phe	Met	Glu	Ile	Thr	Glu	Lys	Ile
65					70					75					80
Gln	Met	Ala	Ser	Asp	Asn	Thr	Asn	Asp	Leu	Ile	Gln	Ser	Gly	Val	Asn
				85					90					95	
Thr	Arg	Leu	Leu	Thr	Ile	Gln	Ser	His	Val	Gln	Asn	Tyr	Ile	Pro	Ile
			100					105					110		
Ser	Leu	Thr	Gln	Gln	Met	Ser	Asp	Leu	Arg	Lys	Phe	Ile	Ser	Glu	Ile
		115					120					125			
Thr	Ile	Arg	Asn	Asp	Asn	Gln	Glu	Val	Leu	Pro	Gln	Arg	Ile	Thr	His
	130					135					140				
Asp	Val	Gly	Ile	Lys	Pro	Leu	Asn	Pro	Asp	Asp	Phe	Trp	Arg	Cys	Thr
145					150					155					160
Ser	Gly	Leu	Pro	Ser	Leu	Met	Lys	Thr	Pro	Lys	Ile	Arg	Leu	Met	Pro
				165					170					175	
Gly	Pro	Gly	Leu	Leu	Ala	Met	Pro	Thr	Thr	Val	Asp	Gly	Cys	Ile	Arg
			180					185					190		
Thr	Pro	Ser	Leu	Val	Ile	Asn	Asp	Leu	Ile	Tyr	Ala	Tyr	Thr	Ser	Asn
		195					200					205			
Leu	Ile	Thr	Arg	Gly	Cys	Gln	Asp	Ile	Gly	Lys	Ser	Tyr	Gln	Val	Leu
		210				215					220				
Gln	Ile	Gly	Ile	Ile	Thr	Val	Asn	Ser	Asp	Leu	Val	Pro	Asp	Leu	Asn
225					230					235					240
Pro	Arg	Ile	Ser	His	Thr	Phe	Asn	Ile	Asn	Asp	Asn	Arg	Lys	Ser	Cys
				245					250					255	
Ser	Leu	Ala	Leu	Leu	Asn	Thr	Asp	Val	Tyr	Gln	Leu	Cys	Ser	Thr	Pro
		260						265					270		
Lys	Val	Asp	Glu	Arg	Ser	Asp	Tyr	Ala	Ser	Ser	Gly	Ile	Glu	Asp	Ile
		275					280					285			
Val	Leu	Asp	Ile	Val	Asn	Tyr	Asp	Gly	Ser	Ile	Ser	Thr	Thr	Arg	Phe
		290				295					300				
Lys	Asn	Asn	Asn	Ile	Ser	Phe	Asp	Gln	Pro	Tyr	Ala	Ala	Leu	Tyr	Pro
305					310					315					320
Ser	Val	Gly	Pro	Gly	Ile	Tyr	Tyr	Lys	Gly	Lys	Ile	Ile	Phe	Leu	Gly
				325					330					335	
Tyr	Gly	Gly	Leu	Glu	His	Pro	Ile	Asn	Glu	Asn	Val	Ile	Cys	Asn	Thr
			340					345					350		

[illegible]











Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys  
515 520 525

Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn  
530 535 540

Ile Met Ile Thr Thr Ile Ile Ile Glu Ile Ile Val Ile Leu Leu Ser  
545 550 555 560

Leu Ile Ala Val Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro  
565 570 575

Val Thr Leu Ser Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe  
580 585 590

Ser Asn

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 920 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGCAAACATG	TCCAAAAACA	AGGACCAACG	CACCGCTAAG	ACACTAGAAA	AGACCTGGGA	60
CACTCTCAAT	CATTTATTAT	TCATATCATC	GGGCTTATAT	AAGTTAAATC	TTAAATCTGT	120
AGCACAAATC	ACATTATCCA	TTCTGGCAAT	GATAATCTCA	ACTTCACTTA	TAATTACAGC	180
CATCATATTC	ATAGCCTCGG	CAAACCACAA	AGTCACACTA	ACAACTGCAA	TCATACAAGA	240
TGCAACAAGC	CAGATCAAGA	ACACAACCCC	AACATACCTC	ACTCAGGATC	CTCAGCTTGG	300
AATCAGCTTC	TCCAATCTGT	CTGAAATTAC	ATCACAAACC	ACCACCATAC	TAGCTTCAAC	360
AACACCAGGA	GTCAAGTCAA	ACCTGCAACC	CACAACAGTC	AAGACTAAAA	ACACAACAAC	420
AACCCAAACA	CAACCCAGCA	AGCCCACTAC	AAAACAACGC	CAAAACAAAC	CACCAAACAA	480
ACCCAATAAT	GATTTTCACT	TCGAAGTGTT	TAACTTTGTA	CCCTGCAGCA	TATGCAGCAA	540
CAATCCAACC	TGCTGGGCTA	TCTGCAAAAG	AATACCAAAC	AAAAAACCAG	GAAAGAAAAC	600
CACCACCAAG	CCTACAAAAA	AACCAACCTT	CAAGACAACC	AAAAAAGATC	TCAAACCTCA	660
AACCACTAAA	CCAAAGGAAG	TACCCACCAC	CAAGCCCACA	GAAGAGCCAA	CCATCAACAC	720



Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe  
 195 200 205  
 Lys Thr Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu  
 210 215 220  
 Val Pro Thr Thr Lys Pro Thr Glu Glu Pro Thr Ile Asn Thr Thr Lys  
 225 230 235 240  
 Thr Asn Ile Thr Thr Thr Leu Leu Thr Asn Asn Thr Thr Gly Asn Pro  
 245 250 255  
 Lys Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr Ser Ser Glu Gly  
 260 265 270  
 Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro Ser Gln  
 275 280 285  
 Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln  
 290 295

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATCAATCAAA GGTCCTGTGA TAATAG

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATGACTTGA TAATGAG

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

00475416-010700

[illegible]

AATTCATGGA GTTGCTAATC CTCAAAGCAA ATGCAATTAC CACAATCCTC ACTGCAGTCA 60  
CATTTCGTTT TGCTTCTGGT TCTAAG 86

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ACTGGCATCA ATCTAGCACT ACATGAG 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

AATTCATGCC	AACTTTTAATA	CTGCTAATTA	TTACAACAAT	GATTATGGCA	TCTTCCTGCC	60
AAATAGATAT	CACAAAATA	CAGCATGTAG	GTGTATTGGT	CAACAGTCCC	AAAGGGATGA	120
AGATATCACA	AAACTT					136

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTTC 60

GTAACAGTTT TGTAATAAAA AAACCTATAA ATAG 94

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTTC 60

GTAACAGTTT TGTAATAAAA AAACCTATAA ATATTCCGGA ATTCAGATCT GCAGCGGCCG 120

CTCCATCTAG AAGGTACCCG G 141

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGACTAAT TCCATCAAAA GTGAAAAGGC T 31

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAAGAAAAAG GAATAAAA 18

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:

00475460-01000









- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGAATACT	GGAAGCATAC	CAATCACGGA	AAGGATGCTG	GCAATGAGCT	GGAGACGTCC	60
ATGGCTACTA	ATGGCAACAA	GCTCACCAAT	AAGATAACAT	ATATATTATG	GACAATAATC	120
CTGGTGTTAT	TATCAATAGT	CTTCATCATA	GTGCTAATTA	ATTCCATCAA	AAGTGAAAAG	180
GCTCATGAAT	CATTGCTGCA	AGACATAAAT	AATGAGTTTA	TGGAAATTAC	AGAAAAGATC	240
CAAATGGCAT	CGGATAATAC	CAATGATCTA	ATACAGTCAG	GAGTGAATAC	AAGGCTTCTT	300
ACAATTCAGA	GTCATGTCCA	GAATTATATA	CCAATATCAC	TGACACAACA	GATGTCAGAT	360
CTTAGGAAAT	TCATTAGTGA	AATTACAATT	AGAAATGATA	ATCAAGAAGT	GCTGCCACAA	420
AGAATAACAC	ATGATGTGGG	TATAAAACCT	TTAAATCCAG	ATGATTTTTG	GAGATGCACG	480
TCTGGTCTTC	CATCTTTAAT	GAAAACTCCA	AAAATAAGGT	TAATGCCAGG	GCCGGGATTA	540
TTAGCTATGC	CAACGACTGT	TGATGGCTGT	ATCAGAACTC	CGTCCTTAGT	TATAAATGAT	600
CTGATTTATG	CTTATACCTC	AAATCTAATT	ACTCGAGGTT	GTCAGGATAT	AGGAAAATCA	660
TATCAAGTCT	TACAGATAGG	GATAATAACT	GTAAACTCAG	ACTTGGTACC	TGACTTAAAT	720
CCCAGGATCT	CTCATACTTT	TAACATAAAT	GACAATAGGA	AGTCATGTTC	TCTAGCACTC	780
CTAAATACAG	ATGTATATCA	ACTGTGTTCA	ACTCCCAAAG	TTGATGAAAG	ATCAGATTAT	840
GCATCATCAG	GCATAGAAGA	TATTGTACTT	GATATTGTCA	ATTATGATGG	CTCAATCTCA	900
ACAACAAGAT	TTAAGAATAA	TAACATAAGC	TTTGATCAAC	CTTATGCTGC	ACTATACCCA	960
TCTGTTGGAC	CAGGGATATA	CTACAAAGGC	AAAATAATAT	TTCTCGGGTA	TGGAGGTCTT	1020
GAACATCCAA	TAAATGAGAA	TGTAATCTGC	AACACAACCTG	GGTGTCCCGG	GAAAACACAG	1080
AGAGACTGCA	ATCAGGCATC	TCATAGTCCA	TGGTTTTTCAG	ATAGGAGGAT	GGTCAACTCT	1140
ATCATTGTTG	TTGACAAAGG	CTTAAACTCA	ATTCCAAAAT	TGAAGGTATG	GACGATATCT	1200
ATGAGACAGA	ATTACTGGGG	GTCAGAAGGA	AGGTTACTTC	TACTAGGTAA	CAAGATCTAT	1260
ATATATACAA	GATCCACAAG	TTGGCATAGC	AAGTTACAAT	TAGGAATAAT	TGATATTACT	1320
GATTACAGTG	ATATAAGGAT	AAAATGGACA	TGGCATAATG	TGCTATCAAG	ACCAGGAAAC	1380

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

27

(2) INFORMATION FOR SEO ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACGGTTGA	AATTATGACG	ATTAATAATG	TTGTTACTAA	TACCGTAGAA	GGACGGTTTA	60
TCTATAGTGT	TTTGATGTCG	TACATCCACA	TAACCAGTTG	TCAGGGTTTC	CCTACTTCTA	120
TAGTGTTTTG	AAGCTT					136

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TAGTACCTCT ATTAATTTTA CTATTGGTAG AGCGTTTATT TATTCATAAA ATGACAAAAG 60  
CATTGTCAAA ACATTATTTT TTTGGATATT TATCTTAA 98

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:





AGGACAAAAG

10

09473240.010700